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OM protein - protein search, using sw model

Run on: June 9, 2003, 07:06:05 ; Search time 28 Seconds (without alignments) 1294.381 Million cell updates/sec

Table: US-10-091-628-2

Perfect score: 1979

Sequence: 1 MRANCSSACPANSSEBELL.....PGPMDCRHALBPVGHITSCE 377

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

ched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database: PIR 73.1

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Result No.	Score	Query Match	Length	DB ID	Description
1	884	44.7	348	2 A49876	Na+-dependent bile acid transporter, ileal - Golden hamster
2	860	43.5	348	2 A49876	Na+-dependent bile acid transporter, ileal - Golden hamster
3	559.5	28.3	362	2 A41601	Na+/taurocholate cotransporter, ileal
4	553	27.9	349	2 I55601	Na+/taurocholate cotransporter, ileal
5	333.5	16.9	477	2 S01696	Na+/taurocholate cotransporter, ileal
6	325	16.4	321	2 B68902	Na+/taurocholate cotransporter, ileal
7	301.5	15.2	305	2 D90031	Na+/taurocholate cotransporter, ileal
8	299.5	15.1	318	2 AD2295	Na+/taurocholate cotransporter, ileal
9	299.5	15.1	323	2 B83757	Na+/taurocholate cotransporter, ileal
10	284	14.4	338	2 T0645	Na+/taurocholate cotransporter, ileal
11	266.5	13.6	311	2 B81236	Na+/taurocholate cotransporter, ileal
12	266.5	13.5	315	2 B81168	Na+/taurocholate cotransporter, ileal
13	265.5	13.4	315	2 B81937	Na+/taurocholate cotransporter, ileal
14	257.5	13.0	297	2 D81438	Na+/taurocholate cotransporter, ileal
15	250	12.6	297	2 E70482	Na+/taurocholate cotransporter, ileal
16	238.5	12.1	292	2 S75443	Na+/taurocholate cotransporter, ileal
17	223	11.3	207	2 G98166	Na+/taurocholate cotransporter, ileal
18	223	11.3	207	2 AH3120	Na+/taurocholate cotransporter, ileal
19	222.5	11.2	318	2 G81995	Na+/taurocholate cotransporter, ileal
20	219.5	11.1	298	2 AF2462	Na+/taurocholate cotransporter, ileal
21	180.5	9.1	182	2 I55222	Na+/taurocholate cotransporter, ileal
22	171	8.6	460	2 T04579	Na+/taurocholate cotransporter, ileal
23	156	7.9	379	2 T06610	Na+/taurocholate cotransporter, ileal
24	142	7.2	344	2 T34981	Na+/taurocholate cotransporter, ileal
25	125	6.3	409	2 I40489	Na+/taurocholate cotransporter, ileal
26	121.5	6.1	324	2 H72285	Na+/taurocholate cotransporter, ileal
27	121	6.1	612	2 T40506	Na+/taurocholate cotransporter, ileal
28	120	6.1	716	2 AB1070	Na+/taurocholate cotransporter, ileal
29	117	5.9	721	2 S56580	Na+/taurocholate cotransporter, ileal

ALIGNMENTS

RESULT 1

A49876

Na+-dependent bile acid transporter, ileal - Golden hamster

C;Species: Mesocricetus auratus (golden hamster)

C;Date: 30-Jun-1995 #sequence_change 05-Nov-1999

C;Accession: A49876

R. Wong, M.H.; Oelkers, P.; Craddock, A.L.; Dawson, P.A.

Artificial expression of the hamster ileal sodium-dependent bile acid transporter, and characterization of the hamster ileal sodium-dependent bile acid transporter, ileal - Golden hamster

A;Reference number: A49876; PMID:9288599

A;Accession: A49876

A;Status: Preliminary

A;Molecule type: mRNA

A;Cross-references: GB:U02028; NID:9455032; PIDN:AAA18640.1; PID:9455033

C;Keywords: transmembrane protein

Query Match 44.7%; Score 884; DB 2; Length 348;

Best Local Similarity 46.9%; Pred. No. 2.6e-65;

Matches 164; Conserv. 74; Mismatches 102; Indels 10; Gaps 4;

Qy 7 SSSACPANS -EELPVGLEVHGN -LELFVFTVYSTVMGCLMPLGCSEVIRKLMWSI 62

Db 3 NSSINCPNATICEGDBSCIAPPSNFAILSPLVYVSMSTVILAVLUMSMGCVNLHFLGLH 62

Qy 63 RRPWGIAGVHLICQFQIMPFTAYLLAISLSPKVOIAVLLIMGCCCGTISNIFTWVQDG 122

Db 63 RRPWGIAGVHLICQFQIMPFTAYLLAISLSPKVOIAVLLIMGCCCGTISNIFTWVQDG 122

Qy 123 MDLSISMTTCSVTVAIGMPPICYIYTWSNLSQQNLTIPYONIGITLVCUTIPVAFGVYY 182

Db 123 MDLSISMTTCSVTVAIGMPPICYIYTWSNLSQQNLTIPYONIGITLVCUTIPVAFGVYY 182

Qy 183 NYRPWQSKTILLKIGAVVGGYIILLYVAVAGVYLAKGWSNSDITLUTISFIPPLIGHTVTGF 242

Db 183 NYRPWQSKTILLKIGAVVGGYIILLYVAVAGVYLAKGWSNSDITLUTISFIPPLIGHTVTGF 242

Qy 183 NHKWPORAKILKISIAGAIIIVLAVVGGIYLQSAWTIPLKWLWLTGTYIAGVGLGF 242

Db 243 LIALFTQHQRCTISLETGQAONIQMCITMQLQSLFTAEHLVQMSLSPPLAYGLFQLIDGF 302

Qy 243 PLARLAGQPWYRCRVALETQGLQNTQLCSTIVQLSPSFSPEDLNLVTFPLTYSIPQIAFAA 302

Db 303 LIVAAVQTYKRLKNGKNSGCTEVCHPRKS -TSSRETNNALEVNEE 350

Qy 303 ILLGAYAYKK ---CHGRONTTEQKTDNEPSSFQETNKGGQFQDKE 348

Db 303 ILLGAYAYKK ---CHGRONTTEQKTDNEPSSFQETNKGGQFQDKE 348

RESULT 2

I38655

Na+/taurocholate cotransporter, ileal - human

C;Species: Homo sapiens (man)

C;Date: 01-Mar-1996 #sequence_change 01-Mar-1996

C;Accession: I38655

Wong, M.H.; Oelkers, P.A.
J. Biol. Chem., 270, 272234-1995
A; Title: Identification of a mutation in the ileal sodium-dependent bile acid transporter
A; Reference number: 138655; PMID: 96070831; PMID: 7552981
A; Accession: 138655
A; Status: Preliminary
A; Molecule type: mRNA
A; Residues: 1-348 <RES>
A; Cross-references: BMBL:010417; NID:9263285; PIDN:AA518701; PID:995399
A; Experimental source: Crohn's disease patient (heterozygous)
A; Note: the wild type is shown; a form with 290-Ser was deficient in transport activity
C; Genetics:
A; Gene: SLC15-A2

Query Match 43.5; Score 860.5; DB 2; Length 348;
Best Local Similarity 45.6%; Pred. No. 2.2e-63;
Matches 160; Conservative 68; Mismatches 104; Indels 19; Gaps 4;

RESULT 4
155601
Na/taurocholate cotransporting polypeptide - human
C; Species: Homo sapiens (man)
C; Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C; Accession: 155601
B; Hagenbuch, B.; Meier, P.J.
J. Clin. Invest., 92, 1265-1314, 1994
A; Title: Molecular cloning, chromosomal localization, and functional characterization of
A; Reference number: 155601; PMID: 9417985; PMID: 8132774
A; Accession: 155601
A; Status: preliminary; translated from GB/EMBL/DBJ
A; Molecule type: mRNA
A; Residues: 1-49 <RES>
A; Cross-references: GDB: L21893; PIDN: AAA36381.1; PID: 9410214
A; Genetics:
A; Gene: SLC10A1; NTCP
A; Cross-references: GDB: 344932; OMIM: 182396
A; Map position: 14pter-14qter

Query Match 27.9%; Score 553; DB 2; Length 349;
Best Local Similarity 36.0%; Pred. No. 4.7e-38;
Matches 124; Conservative 77; Mismatches 109; Indels 34; Gaps 10;
Db 185 KWFQKAKILKIGAVVCGVLLVAVAGVVLAKGSNSDITLITISFIFLIGHYTFLL 244
Db 125 LSYSMTICSTLLAGMELCLLITKWDGSSIVIPYDNIGTSIVLAVVPPVSIGMFVNH 184
Db 125 LSYSMTICSTLLAGMELCLLITKWDGSSIVIPYDNIGTSIVLAVVPPVSIGMFVNH 184
Db 185 RWPQSKILKIGAVVCGVLLVAVAGVVLAKGSNSDITLITISFIFLIGHYTFLL 244
Db 185 RWPQSKILKIGAVVCGVLLVAVAGVVLAKGSNSDITLITISFIFLIGHYTFLL 244
Db 305 VAYQTYKRLKRNKGKNSGTEVCHTRKSTSRETNAFLEVNEGATP 355
Db 245 ARTAGLPYRCKTVAETGMQNTLQLCSTIVLPPENVYFTPLIYTFQ 304
Db 305 LGFYVAKK---CHGKQKAEIPE---SKENGTEPESSFYKAN--GGFQP 345

RESULT 5
A41601
Na/taurocholate transport protein - rat
C; Species: Rattus norvegicus (Norway rat)
C; Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Feb-1997
C; Accession: A41601
B; Hagenbuch, B.; Foguet, M.; Luebbert, H.; Meier, P.J.
J. Biol. Chem., 270, 272234-1995
C; Title: Functional expression cloning and characterization of the hepatocyte Na(+) /bile
A; Reference number: A41601; PMID: 92073340; PMID: 1961729
A; Accession: A41601
A; Status: Preliminary
A; Molecule type: mRNA
A; Residues: 1-362 <RES>
A; Cross-references: GB: M77429
C; Keywords: transmembrane protein

Query Match 28.3%; Score 559.5; DB 2; Length 362;
Best Local Similarity 37.2%; Pred. No. 1.4e-38;
Matches 133; Conservative 69; Mismatches 125; Indels 21; Gaps 9;

RESULT 6
S01696
Gene P3 protein - human
C; Species: Homo sapiens (man)
C; Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 05-Nov-1999
C; Accession: S01696
R; Alcalay, M.; Tonolo, D.
Nucleic Acids Res., 16, 9527-9543, 1988

Query 10 ACPANSSEELPVGLEYGNLLEVFTVSTVNGLMSLGCSEVIRKLNWIRRPWGA 69
Db 7 SADENFS--LPPFGF-TRATDKALSLVLMILLIISLGTMEPSKIAHLWPKGV 62

Query 70 VGLLCQFQIMPFTAYLIAISFSIKPVQIAVJLIMGCCPGGTISNIFFWVQGDMDSIM 129
Db 63 VALVAQFQIMPAAFLWCKIFHLSNIEALAILIJCSPGGNISNLFLAMKGDMNLSIM 122

Query 130 TTCSTVAGLMPCLIVYT--WSWSIQLQNLTIPYQIGTIVLCLTIPVAFGTVNRYW 186

Title: CpG islands of the X chromosome are gene associated.
Reference number: S01696; MUID:89041548; PMID:3186440

Title: Cpg islands of the X chromosome are gene associated.	
Reference: S01696 ; MUIID:89041548 ; PMID:3186440	
Accession: S01696	
Molecule type: DNA	
Residues: 1-477 <ALC>	
Cross-references: EMBL:X12458; NID:935187; PID:935188	
Query Match 16.9% ; Score: 333.5 ; DB 2; Length 477;	
Best Local Similarity 31.5% ; Prod: 7.6e-20 ; Mismatches 115 ; Indels 21 ; Gaps 3 ; Matches 87 ; Conservative 53 ;	
1.2 PANSEEELPVGLEVHGNLRLVTVVSVTMMGLMSSIGCSVEIRKLWSHIRRP#GAVG 71	
1.72 PAEPTATLSDADIAHESPNPILYLLPLIFVNKCSF -GCKYTELEVKGMLMSPQPNLGLG 229	
7.2 LLOCGLMPPTAVLLAISLSSLKPVQAVAILVINGCPGGTISNIIFTPWGDMDLSISMTT 131	
23.0 LLOCFLVNPILYALMVKMFLPKALQLLIMCSPSGGSLFSLGGDVTIALSMTF 289	
13.2 CSTVAALGMPCLCYLTVWSLQONLTIPYQONIGRTVCLPVAFQVYNYRWPQSK 191	
230 LSTVAATGFLPLSSATISRLLSIHTELVPSKILGTLFIAPIAVGVLKSLRKPFSQ 349	
19.2 IILKIGAVVGCVLL-----VVAVAGVVLAKGSWSNDTLLTISFPLIGHTG 241	
35.0 LLIQVVKPESFVLLGGFLAYRNGVFLLAGRL-----PIVLVGITYPLVHVG 400	
24.2 FLLALFTFQSQRCTISLETGQONICMQLQS 277	
40.1 YCATCCKLPLVAQRRTVSVIEGVQNSLILAMQLQS 436	
RESULT 6	
9902 probable sodium-dependent transporter yocs - Bacillus subtilis	
Species: Bacillus subtilis	
Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000	
Accession: E69902	
Kunst, F.; Broekaert, N.; Mosser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berteletti, J.; Bron, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chodat, P.; Konigstein, G.; Krog, H.; Kurita, M.; Kurita, K.; Lardinois, A.; Manoel, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, M.; Rivoira, C.; Roche, B.; Rose, M.; Sadai, Y.; Sato, T.; Scanlon, S.; Schleich, S.; Schroeter, R.; Sofrone, P.; Sekine, J.; Sekowska, A.; Seror, Euchi, M.; Tamashiro, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, Y.; Winters, P.; Wipat, A.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshida, K.	
Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, M.; Rivoira, C.; Roche, B.; Rose, M.; Sadai, Y.; Sato, T.; Scanlon, S.; Schleich, S.; Schroeter, R.; Sofrone, P.; Sekine, J.; Sekowska, A.; Seror, Euchi, M.; Tamashiro, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, Y.; Winters, P.; Wipat, A.; Yamane, K.; Yamamoto, K.; Yata, K.; Yoshida, K.	
Title: The complete genome sequence of the Gram-positive bacterium <i>Bacillus subtilis</i> . Reference number: A95980 ; MUIID:9804033 ; PMID:938377	
Accession: E69902	
Status: preliminary; nucleic acid sequence not shown; translation not shown	
Molecule type: DNA	
Residues: 1-321 <KUN>	
Cross-references: GB:Z999114; GB:AL009126; NID:92634230; PID:92634238	
Experimetal source: strain 168	
Genetics: Gene: yocs	
Superfamily: Bacillus subtilis sodium-dependent transporter yocs	
Query Match 16.4% ; Score: 325; DB 2; Length 321;	
Best Local Similarity 27.6% ; Prod: 2.0e-19 ; Mismatches 114 ; Indels 30 ; Gaps 12 ; Matches 84 ; Conservative 76 ;	
3.3 VFTVVS--TVMGGLMSSLGCSVEIRKLWSHIRRP#GAVGILCQFGLMPFTAYLIAIS 89	
32 LFWIWSSTVITIELGIMCMGLTIQADDFKEVLRKPWQVQIVGQTYIMPLVAFGLFG 91	
RESULT 8	
AD3295 sodium/bile acid cotransporter homolog, sbf Family BME10346 [Imported] - Bruce C;Species: Brucella melitensis	
C;Accession: AD3295 - Feb-2002 #sequence_revision 01-Feb-2002	
90 FSLKPVQVAVLIMGCCPGGTISNIETWDGMDLSISMTTCAVAGMMPCLTYT 149	

RESULTS 9

R; DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, N.; Mazur, M.; Goitsman, E.; Selkov, E.; Blazquez, P.H.; Hagiwara, S.; O'Callaghan, D.; Letessier, A; Reference number: AD3252; PMID:11756688

A; Cross-references: GB:AP001510; PIDN:AA51527.1; PID:917982244; GSPDB:GN00190

A; Experimental source: strain 16M

C; Genetics:

A; Gene: BME10346

A; Map position: I

C; Superfamily: *Bacillus subtilis* sodium-dependent transporter yocs

Query Match 15.1%; Score 299.5; DB 2; Length 318;

Best Local Similarity 27.9%; Pred. No. 3.2e-17;

Matches 79; Conservative 66; Mismatches 117; Indels 21; Gaps 7;

RESULTS 10

T02645

Query Match 15.1%; Score 299.5; DB 2; Length 318;

Best Local Similarity 27.9%; Pred. No. 3.2e-17;

Matches 79; Conservative 66; Mismatches 117; Indels 21; Gaps 7;

hypothetical protein At2g26900 [imported] - *Arabidopsis thaliana*

35 IAPPIWVLLGIMFGMGLTISGKDFAEVAKRPFDAVGLVQDFIMPLAVLILPPIPM 94

93 KPVQIAVWIMGCGPCTISNLTPEWWDGMDLISITTCSTVAALGMMPLCIVLYTWSW 152

95 SPPVAAAGTIVLGCGGTASNYMTPSGDVALSVACTSVTTLAPITVTPFLWMPFA--- 151

153 SLOQNLITPYQNYQIGITLV-CLITPVAVGTYVNYRWP--KQSKIIKIGAVVGGVLL-- 206

152 --SQQLPDAMSMFISITVTKVPLALGEVFLQKLVPEVKAAPVMLPLPSVYGVIVAA 209

207 WAWAGVYTLAKGSWNSDTLITISFPLIGHTFLALFTHOSWRCRTISLETGQN 266

210 WAWVNAKAAQ---SGLIFAVVVLNCIGLLGYPARFAGLSLAKRKASISIEVMQN 265

267 IQMCITMQLQLSFTAEHLYQMLSPFLA-YGLFLQDGFILVAY 308

266 ----SGLGAAGLGNHFSPLAALPAIFSVWHNTISGPVLVSIW----- 304

RESULTS 11

T02645

Query Match 15.1%; Score 299.5; DB 2; Length 318;

Best Local Similarity 27.9%; Pred. No. 3.2e-17;

Matches 79; Conservative 66; Mismatches 117; Indels 21; Gaps 7;

hypothetical protein At2g26900 [imported] - *Arabidopsis thaliana*

C; Species: *Arabidopsis thaliana* (mouse-ear cress)

C; Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001

R; Rounsley, S.D.; Ronning, C.M.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sy submitted to the EMBL Data Library, August 1998

A; Description: *Arabidopsis thaliana* chromosome 11 BAC F12C20 genomic sequence.

A; Reference number: Z14685

A; Accession: T02645

A; Molecule type: DNA

A; Residues: 1-338 <ROU>

A; Cross-references: EMBL:AC005168; NID:91426033; PID:3426051

A; Experimental source: cultivar Columbia

R; Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.B.; Umayam, L.; Fallon, L.; Euse, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999

A; Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A; Reference number: A84420; MUID:20083487; PMID:10617197

A; Accession: C84666

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-138 <STO>

A; Cross-references: GB:AE002093; NID:91426051; PIDN:AA51527.1; GSPDB:GN00139

C; Genetics:

A; Gene: AT2g26900; F12C20.6

A; Map position: 2

A; Introns: 22/2; 61/3; 99/3; 120/3; 163/2; 190/3; 208/1; 240/3; 293/3

Query Match 14.4%; Score 284; DB 2; Length 338;

Best Local Similarity 25.8%; Pred. No. 6.4e-16;

Matches 80; Conservative 54; Mismatches 120; Indels 56; Gaps 8;

RESULTS 12

B83757

Query Match 15.1%; Score 299.5; DB 2; Length 323;

Best Local Similarity 24.8%; Pred. No. 3.2e-17;

Matches 80; Conservative 80; Mismatches 122; Indels 41; Gaps 9;

sodium-dependent transporter BH0858 [imported] - *Bacillus halodurans* 4(strain C-125)

C; Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C; Accession: B83757

R; Takami, H.; Nakagawa, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira Nucleic Acids Res. 28, 4317-4331, 2000

C; Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and reference number: AB3650; MUID:20512582; PMID:11058132

A; Accession: B83757

A; Molecule type: DNA

A; Residues: 1-323 <STO>

A; Cross-references: GB:AP001510; PIDN:BA04577.1; GSPDB:GN00139

C; Genetics:

C; Superfamily: *Bacillus subtilis* sodium-dependent transporter yocs

Query Match 15.1%; Score 299.5; DB 2; Length 323;

Best Local Similarity 24.8%; Pred. No. 3.2e-17;

Matches 80; Conservative 80; Mismatches 122; Indels 41; Gaps 9;

RESULTS 13

34 FTVVS--TVMGGLMPSLGCSVIRKWLSHIRRPGWVAVGLCQGFLMPFTAYLLAISF 90

33 FTVTPHPTTLLGIVMFGNLTKLSDPRVILQKPIPLVGLAOFVIMPLVAFALAYAF 92

91 SLPVQATAVLIMGCCPGTISNITFTWVGDMDLTSMTTCTVAALGMMPLCIVLYTW 150

93 NLPPELARGLVLVGACPGTATSNMVYLAKGNAVAAMTSVSTMALPAPITVFFILLAG 152

RESULTS 14

QY 151 SWSLQNLITPYQNYQIGITLV-CLTPVAVGTYVNYRWPK---QSKIIKIGAVVGGVLL 206

Db 153 QW----LPIDAKANFVSIQMIITPIALGFLVIRMAPNAVDKSTAVLPLVISV AIMAI 206

Qy 207 VVAVGVLAKGSWNSDTLITISFPLIGHTFLALFTHQWQRCFTISLETGQN 266

Db 207 VSAVYGAQANLMSGAALLFLAV-MIHNFGLLGUYTAKFVGLDESTRAISIVGMQ 265

Qy 267 IQMCITMQLQISFTABHLVQNLISFPA---SLGFLQIOLINGFLVAYAQYKRELLNKHGRKNSG 325

Db 266 ----SGLGAAGLGNHFSPLAALPAIFSVWHNTISGPVLVSIW----- 304

Qy 326 CTEVCHTRKSTSSRETNAFLEV 348

Db 305 ----RSAKSAQKRSQSDADRKVD 322

RESULTS 15

QY 151 SWSLQNLITPYQNYQIGITLV-CLTPVAVGTYVNYRWPK---QSKIIKIGAVVGGVLL 206

Db 153 QW----LPIDAKANFVSIQMIITPIALGFLVIRMAPNAVDKSTAVLPLVISV AIMAI 206

Qy 207 VVAVGVLAKGSWNSDTLITISFPLIGHTFLALFTHQWQRCFTISLETGQN 266

Db 207 VSAVYGAQANLMSGAALLFLAV-MIHNFGLLGUYTAKFVGLDESTRAISIVGMQ 265

Qy 267 IQMCITMQLQISFTABHLVQNLISFPA---SLGFLQIOLINGFLVAYAQYKRELLNKHGRKNSG 325

Db 266 ----SGLGAAGLGNHFSPLAALPAIFSVWHNTISGPVLVSIW----- 304

Qy 326 CTEVCHTRKSTSSRETNAFLEV 348

Db 305 ----RSAKSAQKRSQSDADRKVD 322

Qy 258 ISLETCAGIONCITMLQLSFTAELHYQMLSFPLA-YGLFQOLIDFELIVAAAYQTYKRRKL 316
 Db 257 LALEVGMQNSGLAAALAAAHFA--VAFFVAVGALPSWHRNISGSLIA---TYWAAKA 309
 Qy 317 NRKGK 321
 Db 310 GRHKK 314

RESULT 14
 D83438 Probable transporter PA1650 [imported] - *Pseudomonas aeruginosa* (strain PA01)
 C;Species: *Pseudomonas aeruginosa*
 C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
 C;Accession: D83438
 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen reference number: A82950; PMID:20437337; PMID:10984043
 A;Cross-references: GB:AE004593; GB:AB004091; NID:9947619; PIDN:AAG05039.1; GSPDB:GN001
 A;Molecule type: DNA
 A;Status: preliminary
 A;Experimental source: strain PA01
 A;Gene: PA1650
 C;Superfamily: *Bacillus* subtilis sodium-dependent transporter yocs
 C;Genetics:
 A;Gene: sbf
 C;Superfamily: *Bacillus* subtilis sodium-dependent transporter yocs

Query Match 12.6%; Score 250; DB 2; Length 297;
 Best Local Similarity 26.0%; Pred. No. 3.5e-13;
 Matches 81; Conservative 64; Mismatches 126; Indels 40; Gaps 10;

Qy 29 NLELVPTVSVTMMGGLI-----MFSLGCSVIRKLWSHIRPWRGIA 69
 Db 3 DFSFLILIVSLSLGLPPEFANLKLPLPLVITIMSLMGLTPEDFKIRKARPKIVF 62
 Qy 70 VGLLCQFGLMPTAYLLAISFLSKPQIAAVLIMGCCPGGTISNIFTEWVGDMDLSISM 129
 Db 63 YGALIOTYVMPLSGVLISKFLPPLLVGVLVGSAPGGTASNLTYSRGLDSYSIM 122
 Qy 130 TTCSCTVAALGMMPLCYLYTWSLQONLTIPYQNI-GITLVCLTIPVAFV---YVNY 184
 Db 123 TTTSFLSLSPFLPTPLWTVLLAGKY----VEVPFLSMFETTLKIVTVPLGMVLRFLRY 177
 Qy 185 RWPKQSKTILKIGAVGGVLLVVAAGWLAKGSNSDTLULTSFIFPLIGHTTGFLL 244
 Db 178 QINKEVK-FLPFLAVFS-ISLIIAVIFALNSKLKELSFVLSVLIHNVLGFLGILP 234
 Qy 245 ALFTHQSWSQRCRTISLETGAGNIONCITMLQLSFTAELHYQMLSFPLAYGLFQOLIDGFLI 304
 Db 235 GLLAGLDKRYKVALSTEVGMNSGILS-TVIALKYFS----KVSALESA--IFSLSLON-LI 286
 Qy 305 VAAVQTYKRL 315
 Db 287 GVVLSLIFFRL 297

Search completed: June 9, 2003, 07:10:12
 Job time : 30 secs

Qy 33 VFTVVTSTVMMGLIMSLGCSVIRKLWSHIRPWRGIAVGLLTFADFLFVTPKPVLYGQVIVLPLACPLIVQGFL 92
 Best Local Similarity 26.2%; Pred. No. 8.6e-11;
 Matches 75; Conservative 60; Mismatches 128; Indels 23; Gaps 7;

Qy 93 KPYQIAVATLIMGCCPGGTISNIFTEWVGDMDLSISMTCSTVAAIGMMPLCIVLYTWSW 152
 Db 66 EAALAVGMQMLAASPGGTANLYSHLAGDVALNITLAVNSVIALTMLPLIVNL---- 120

Qy 153 SIIQ-----QNLTIPIYQHIGTIVLCLTIPVAGVYVYKWRPROSKILKIGAVVGGVLL 206
 Db 121 SIIQYFMGQCAIPLQFGRKVQVFEVIVLCPVALGMLVNRNLPKAVADRIQKPVKILSAILL 180

Qy 207 VVAVAGVTLAKGSWNDDTLLT----SFIEPLIPLVGHVFLFALFTHQSWSQRCRTSLET 262
 Db 181 VILL-LLAALK-DWQTFTYIAPVGLAALAFNLISLAVGWWPLRKAQAAVAGMEI 237

Qy 263 GAONIQMCITMLQLSFTAELHYQMLSFPLAYGLFQOLIDFELIVAAY 308
 Db 238 GIHNGTLAIA-LAUSPSSLNNSTMAPPAXVGML---FFTAAAF 278

RESULT 15
 E70482 Na(+) dependent transporter (Sbf family) - *Aquifex aeolicus*
 C;Species: *Aquifex aeolicus*
 C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jun-2000
 C;Accession: E70482
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; On V. Nature 392, 353-358, 1998
 A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.
 A;Reference number: A70300; PMID:98196666; PMID:9537320
 A;Accession: E70482
 A;Status: preliminary: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-297 <AQP>
 A;Cross-references: GB:AE000774; NID:92984324; PIDN:AAC07854.1; PID:g2984333; GB:AE00065
 A;Experimental source: strain VPS